

ENTERED



PCT09

## RAW SEQUENCE LISTING

DATE: 07/12/2002

PATENT APPLICATION: US/09/936,035

TIME: 11:16:52

Input Set : N:\Crf3\Datahold\EFS\09936035\gncap01005.txt

Output Set: N:\CRF3\07122002\I936035.raw

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3 <110> APPLICANT: Genetica, Inc.
4     Beach, David H.
5     Hannon, Gregory J.
7 <120> TITLE OF INVENTION: METHODS AND REAGENTS FOR INCREASING PROLIFERATIVE
8     CAPACITY AND PREVENTING REPLICATIVE SENESENCE
10 <130> FILE REFERENCE: GNCA-P01-005
12 <140> CURRENT APPLICATION NUMBER: 09/936,035
13 <141> CURRENT FILING DATE: 1999-11-24
15 <150> PRIOR APPLICATION NUMBER: PCT/US99/27907
16 <151> PRIOR FILING DATE: 1999-11-24
18 <150> PRIOR APPLICATION NUMBER: 60/120,549
19 <151> PRIOR FILING DATE: 1999-02-17
21 <150> PRIOR APPLICATION NUMBER: 60/109,891
22 <151> PRIOR FILING DATE: 1998-11-25
24 <160> NUMBER OF SEQ ID NOS: 43
26 <170> SOFTWARE: PatentIn Ver. 2.1
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 4027
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (57)..(3452)
37 <400> SEQUENCE: 1
38 caggcagcgt ggtcctgctg cgcacgtggg aagccctggc cccggccacc cccgcg atg 59
39                                     Met
40                                     1
42 ccg cgc gct ccc cgc tgc cga gcc gtg cgc tcc ctg ctg cgc agc cac 107
43 Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser His
44         5                10                15
46 tac cgc gag gtg ctg ccg ctg gcc acg ttc gtg cgg cgc ctg ggg ccc 155
47 Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro
48         20                25                30
50 cag gcc tgg cgg ctg gtg cag cgc ggg gac ccg gcg gct ttc cgc gcg 203
51 Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala
52         35                40                45
54 ctg gtg gcc cag tgc ctg gtg tgc gtg ccc tgg gac gca cgg ccg ccc 251
55 Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro
56 50                55                60                65
58 ccc gcc gcc ccc tcc ttc cgc cag gtg tcc tgc ctg aag gag ctg gtg 299
59 Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val
60         70                75                80
62 gcc cga gtg ctg cag agg ctg tgc gag cgc ggc gcg aag aac gtg ctg 347

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63 Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu
64      85      90      95
66 gcc ttc ggc ttc gcg ctg ctg gac ggg gcc cgc ggg ggc ccc ccc gag 395
67 Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu
68      100      105      110
70 gcc ttc acc acc agc gtg cgc agc tac ctg ccc aac acg gtg acc gac 443
71 Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp
72      115      120      125
74 gca ctg cgg ggg agc ggg gcg tgg ggg ctg ctg ttg cgc cgc gtg ggc 491
75 Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly
76 130      135      140      145
78 gac gac gtg ctg gtt cac ctg ctg gca cgc tgc gcg ctc ttt gtg ctg 539
79 Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu
80      150      155      160
82 gtg gct ccc agc tgc gcc tac cag gtg tgc ggg ccg ccg ctg tac cag 587
83 Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln
84      165      170      175
86 ctc ggc gct gcc act cag gcc cgg ccc ccg cca cac gct agt gga ccc 635
87 Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro
88      180      185      190
90 cga agg cgt ctg gga tgc gaa cgg gcc tgg aac cat agc gtc agg gag 683
91 Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu
92      195      200      205
94 gcc ggg gtc ccc ctg ggc ctg cca gcc ccg ggt gcg agg agg cgc ggg 731
95 Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly
96 210      215      220      225
98 ggc agt gcc agc cga agt ctg ccg ttg ccc aag agg ccc agg cgt ggc 779
99 Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly
100      230      235      240
102 gct gcc cct gag ccg gag cgg acg ccc gtt ggg cag ggg tcc tgg gcc 827
103 Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala
104      245      250      255
106 cac ccg ggc agg acg cgt gga ccg agt gac cgt ggt ttc tgt gtg gtg 875
107 His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val
108      260      265      270
110 tca cct gcc aga ccc gcc gaa gaa gcc acc tct ttg gag ggt gcg ctc 923
111 Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu
112      275      280      285
114 tct ggc acg cgc cac tcc cac cca tcc gtg ggc cgc cag cac cac gcg 971
115 Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala
116 290      295      300      305
118 ggc ccc cca tcc aca tcg cgg cca cca cgt ccc tgg gac acg cct tgt 1019
119 Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys
120      310      315      320
122 ccc ccg gtg tac gcc gag acc aag cac ttc ctc tac tcc tca ggc gac 1067
123 Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp
124      325      330      335
126 aag gag cag ctg cgg ccc tcc ttc cta ctc agc tct ctg agg ccc agc 1115
127 Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser

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128				340			345			350							
130	ctg	act	ggc	gct	cgg	agg	ctc	gtg	gag	acc	atc	ttt	ctg	ggt	tcc	agg	1163
131	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu	Gly	Ser	Arg	
132	355						360			365							
134	ccc	tgg	atg	cca	ggg	act	ccc	cgc	agg	ttg	ccc	cgc	ctg	ccc	cag	cgc	1211
135	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	Pro	Gln	Arg	
136	370						375			380			385				
138	tac	tgg	caa	atg	cgg	ccc	ctg	ttt	ctg	gag	ctg	ctt	ggg	aac	cac	gcg	1259
139	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	Asn	His	Ala	
140				390						395			400				
142	cag	tgc	ccc	tac	ggg	gtg	ctc	ctc	aag	acg	cac	tgc	ccg	ctg	cga	gct	1307
143	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	Leu	Arg	Ala	
144	405						410			415							
146	gcg	gtc	acc	cca	gca	gcc	ggt	gtc	tgt	gcc	cgg	gag	aag	ccc	cag	ggc	1355
147	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys	Pro	Gln	Gly	
148	420						425			430							
150	tct	gtg	gcg	gcc	ccc	gag	gag	gag	gac	aca	gac	ccc	cgt	cgc	ctg	gtg	1403
151	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg	Arg	Leu	Val	
152	435						440			445							
154	cag	ctg	ctc	cgc	cag	cac	agc	agc	ccc	tgg	cag	gtg	tac	ggc	ttc	gtg	1451
155	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr	Gly	Phe	Val	
156	450						455			460			465				
158	cgg	gcc	tgc	ctg	cgc	cgg	ctg	gtg	ccc	cca	ggc	ctc	tgg	ggc	tcc	agg	1499
159	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp	Gly	Ser	Arg	
160				470						475			480				
162	cac	aac	gaa	cgc	cgc	ttc	ctc	agg	aac	acc	aag	aag	ttc	atc	tcc	ctg	1547
163	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe	Ile	Ser	Leu	
164	485						490			495							
166	ggg	aag	cat	gcc	aag	ctc	tcg	ctg	cag	gag	ctg	acg	tgg	aag	atg	agc	1595
167	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp	Lys	Met	Ser	
168	500						505			510							
170	gtg	cgg	ggc	tgc	gct	tgg	ctg	cgc	agg	agc	cca	ggg	ggt	ggc	tgt	gtt	1643
171	Val	Arg	Gly	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	Gly	Cys	Val	
172	515						520			525							
174	ccg	gcc	gca	gag	cac	cgt	ctg	cgt	gag	gag	atc	ctg	gcc	aag	ttc	ctg	1691
175	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	Lys	Phe	Leu	
176	530						535			540			545				
178	cac	tgg	ctg	atg	agt	gtg	tac	gtc	gtc	gag	ctg	ctc	agg	tct	ttc	ttt	1739
179	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	Phe	
180				550						555			560				
182	tat	gtc	acg	gag	acc	acg	ttt	caa</									

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194 cgg gaa gcc agg ccc gcc ctg ctg acg tcc aga ctc cgc ttc atc ccc 1931
195 Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro
196 610 615 620 625
198 aag cct gac ggg ctg cgg ccg att gtg aac atg gac tac gtc gtg gga 1979
199 Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly
200 630 635 640
202 gcc aga acg ttc cgc aga gaa aag agg gcc gag cgt ctc acc tcg agg 2027
203 Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg
204 645 650 655
206 gtg aag gca ctg ttc agc gtg ctc aac tac gag cgg gcg cgg cgc ccc 2075
207 Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro
208 660 665 670
210 ggc ctc ctg ggc gcc tct gtg ctg ggc ctg gac gat atc cac agg gcc 2123
211 Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala
212 675 680 685
214 tgg cgc acc ttc gtg ctg cgt gtg cgg gcc cag gac ccg ccg cct gag 2171
215 Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu
216 690 695 700 705
218 ctg tac ttt gtc aag gtg gat gtg acg ggc gcg tac gac acc atc ccc 2219
219 Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro
220 710 715 720
222 cag gac agg ctc acg gag gtc atc gcc agc atc atc aaa ccc cag aac 2267
223 Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn
224 725 730 735
226 acg tac tgc gtg cgt cgg tat gcc gtg gtc cag aag gcc gcc cat ggg 2315
227 Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly
228 740 745 750
230 cac gtc cgc aag gcc ttc aag agc cac gtc tct acc ttg aca gac ctc 2363
231 His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu
232 755 760 765
234 cag ccg tac atg cga cag ttc gtg gct cac ctg cag gag acc agc ccg 2411
235 Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro
236 770 775 780 785
238 ctg agg gat gcc gtc gtc atc gag cag agc tcc tcc ctg aat gag gcc 2459
239 Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala
240 790 795 800
242 agc agt ggc ctc ttc gac gtc ttc cta cgc ttc atg tgc cac cac gcc 2507
243 Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala
244 805 810 815
246 gtg cgc atc agg ggc aag tcc tac gtc cag tgc cag ggg atc ccg cag 2555
247 Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln
248 820 825 830
250 ggc tcc atc ctc tcc acg ctg ctc tgc agc ctg tgc tac ggc gac atg 2603
251 Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met
252 835 840 845
254 gag aac aag ctg ttt gcg ggg att cgg cgg gac ggg ctg ctc ctg cgt 2651
255 Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg
256 850 855 860 865
258 ttg gtg gat gat ttc ttg ttg gtg aca cct cac ctc acc cac gcg aaa 2699

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259 Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys
260      870      875      880
262 acc ttc ctc agg acc ctg gtc cga ggt gtc cct gag tat ggc tgc gtg 2747
263 Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val
264      885      890      895
266 gtg aac ttg cgg aag aca gtg gtg aac ttc cct gta gaa gac gag gcc 2795
267 Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala
268      900      905      910
270 ctg ggt ggc acg gct ttt gtt cag atg ccg gcc cac ggc cta ttc ccc 2843
271 Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro
272      915      920      925
274 tgg tgc ggc ctg ctg ctg gat acc cgg acc ctg gag gtg cag agc gac 2891
275 Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp
276 930      935      940      945
278 tac tcc agc tat gcc cgg acc tcc atc aga gcc agt ctc acc ttc aac 2939
279 Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn
280      950      955      960
282 cgc ggc ttc aag gct ggg agg aac atg cgt cgc aaa ctc ttt ggg gtc 2987
283 Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val
284      965      970      975
286 ttg cgg ctg aag tgt cac agc ctg ttt ctg gat ttg cag gtg aac agc 3035
287 Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser
288      980      985      990
290 ctc cag acg gtg tgc acc aac atc tac aag atc ctc ctg ctg cag gcg 3083
291 Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala
292      995      1000      1005
294 tac agg ttt cac gca tgt gtg ctg cag ctc cca ttt cat cag caa gtt 3131
295 Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val
296 1010      1015      1020      1025
298 tgg aag aac ccc aca ttt ttc ctg cgc gtc atc tct gac acg gcc tcc 3179
299 Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser
300      1030      1035      1040
302 ctc tgc tac tcc atc ctg aaa gcc aag aac gca ggg atg tcg ctg ggg 3227
303 Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly
304      1045      1050      1055
306 gcc aag ggc gcc gcc ggc cct ctg ccc tcc gag gcc gtg cag tgg ctg 3275
307 Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu
308      1060      1065      1070
310 tgc cac caa gca ttc ctg ctc aag ctg act cga cac cgt gtc acc tac 3323
311 Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr
312      1075      1080      1085
314 gtg cca ctc ctg ggg tca ctc agg aca gcc cag acg cag ctg agt cgg 3371
315 Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg
316 1090      1095      1100      1105
318 aag ctc ccg ggg acg acg ctg act gcc ctg gag gcc gca gcc aac ccg 3419
319 Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro
320      1110      1115      1120
322 gca ctg ccc tca gac ttc aag acc atc ctg gac tgatggccac ccgcccacag 3472
323 Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp

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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 07/12/2002  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 2320,2321,2336,2351,2363,2413,2723,2724,2725,2726,3730

Seq#:15; Xaa Pos. 1,2,3

## VARIABLE LOCATION SUMMARY

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Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of &lt;220&gt; to &lt;223&gt; is MANDATORY if n's or Xaa's are present.

in &lt;220&gt; to &lt;223&gt; section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:5; N Pos. 2320,2321,2336,2351,2363,2413,2723,2724,2725,2726,3730

Seq#:15; Xaa Pos. 1,2,3

## VERIFICATION SUMMARY

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Input Set : N:\Crif3\Datahold\EFS\09936035\gncap01005.txt

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L:763 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
L:763 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:2280  
L:764 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
L:764 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:764 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:2340  
L:765 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
L:765 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:765 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:2400  
L:770 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
L:770 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:770 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:2700  
L:787 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
L:787 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:787 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:3720  
L:1119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0